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On protein - protein search, using sw model

Run on: October 9, 2002, 00:24:29 ; Search time 49.62 Seconds  
 (without alignments)  
 367.112 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 164

Sequence: 1 TPVSQTTAAATASVRSRKDP.....TLPPTOALPSSHSSPQQG 164

Scoring table: OLIGO  
 Gapext 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: A\_Geneseq\_032802:\*
- 2: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AJ1980.DAT:\*
- 3: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1982.DAT:\*
- 4: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1983.DAT:\*
- 5: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1984.DAT:\*
- 6: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1985.DAT:\*
- 7: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1986.DAT:\*
- 8: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1987.DAT:\*
- 9: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1988.DAT:\*
- 10: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1989.DAT:\*
- 11: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1990.DAT:\*
- 12: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1991.DAT:\*
- 13: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1992.DAT:\*
- 14: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1993.DAT:\*
- 15: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1994.DAT:\*
- 16: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1995.DAT:\*
- 17: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1996.DAT:\*
- 18: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1997.DAT:\*
- 19: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1998.DAT:\*
- 20: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ1999.DAT:\*
- 21: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ2001.DAT:\*
- 22: /SIDS1/gcdata/geneseq/geneseqp-emb1/AJ2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	154	100.0	164 21 AAY83951	Human mature interleukin-4 immuno
2	164	100.0	192 20 AAW98004	Human interleukin-1 beta
3	164	100.0	194 21 AAY96392	Human IgFMr4 immuno
4	164	100.0	194 21 AAY83985	Full length human
5	139	84.8	197 20 AAW98006	Human interleukin-10
6	137	83.5	137 21 AAY83982	Human interleukin-10
7	97	59.1	161 20 AAW98007	Human interleukin-10
8	48	29.3	113 20 AAW98005	Human interleukin-10
9	47	28.7	21 AAY83983	Human interleukin-10
10	40	24.4	40 20 AAW98008	Human interleukin-10
11	44.6	20	55 20 AAY12716	Human 5' EST secre

## ALIGNMENTS

RESULT ID	1
AY83951	standard; Protein: 164 AA.
AY83951;	
XX	
XX	
DT	28-JUL-2000 (first entry)
XX	Human mature interleukin 18 binding protein,
XX	Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse; KW regulator; drug; sensitivity disease; organ rejection; organ transplant; KW autoimmune disease.
OS	Homo sapiens.
XX	
PN	WO200012555-A1.
PD	09-MAR-2000.
XX	
PF	18-NOV-1998; 98WO-JP01186.
XX	
PR	01-SEP-1998; 98JP-0247588.
PR	18-NOV-1998; 98JP-0327914.
XX	
PA	(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX	
PI	Torigoe K, Taniai M, Kurimoto M;
XX	
DR	WPI; 2000-237850/20.
DR	N-PSB; AAA11002.
PT	Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug

PT for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
 XX  
 PS Claim 1; Page 44-45; 71pp; Japanese.  
 XX  
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant, and in treating autoimmune diseases. This sequence represents the matured human interleukin 12 binding protein.  
 CC  
 CC  
 XX SQ Sequence 164 AA:  
 Query Match 100.0%; Score 164; DB 21; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 5 3e-158; Mismatches 0; Gaps Matches 164; Conservative 0; Indels 0; Gaps  
 Qy 1 IPEVSQMTATASVRSKDPDCSQPPWPAKQCPALFVWAEVEVLNGVLSLSCVACG 60  
 Db 1 tpsqgttaatasavrskdpdcspqppfpaaqcpallevtpewevplngtisvcacs 60  
 Qy 61 RPPNFSTLWLGNGSFTHLPERLWEESTSRSERGSTOTLCKALVIBQLTPALHSTNSFC 120  
 Db 61 rfpnfsllywlgngsfiehlhpgrlwegstsrsengstqtckalviegqtptkpalhstnsfc 120  
 Qy 121 VIVDPEQPVQRNVVLAIDLWAGRATLPTQEALPSSSPQQG 164  
 Db 121 vlvdpqevvqrhvvlqlwagiratlpptqealpssspqgg 164

RESULT	2
ID	AAW98004
XX	AAW98004 standard; Protein; 192 AA.
AC	AAW98004;
XX	
DT	21-JUN-1999 (first entry)
DE	Human interleukin-18 binding protein splice variant IL-18BPa.
KW	Interleukin-18 binding protein; IL-18BP; IL-18BPa; splice variant; human; autoimmune disease; inflammation; diabetes; pancreatitis; rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis; psoriasis; inflammatory bowel disease; multiple sclerosis; ischemic heart disease; ischemic brain injury; therapy.
XX	Homo sapiens.
XX	Key Location/Qualifiers
FH	1..28 /note= "signal peptide"
FT	29..192 /note= "mature protein"
FT	
XX	PN WO9909063-A1.
XX	
PD	25-FEB-1999.
XX	
PF	13-AUG-1998; 98WO-IL00379.
XX	
PR	22-JUL-1998; 98IL-0125463.
PR	14-AUG-1997; 97IL-012554.
PR	27-AUG-1997; 97IL-0121639.
PR	29-SEP-1997; 97IL-0121860.
PR	06-NOV-1997; 97IL-0122134.
XX	
PA	(YEDA ) YEDA RES & DEV CO LTD.
XX	
PI	Dinarello C, Kim SH, Novick D, Rubinstein M;
XX	
DR	WPI; 1999-180975/15.

XX	CC	CC	PT	N-PSDB; AAX24749.
XX	CC	CC	PT	New interleukin-18 binding protein - useful for treating human diseases, including autoimmune disease and inflammation
XX	CC	CC	PS	Claim 3; Page 53-54; 100pp; English.
XX	CC	CC	SQ	The present sequence represents a human interleukin-18 binding protein (IL-18BP) splice variant designated IL-18Bpa. This is one of 4 novel splice variants (see also AAW8005-07); all putative soluble proteins, encoded by cDNA clones (see AAX24749-52) detected following a screening of human peripheral blood monocyte, Jurkat T-cell, peripheral blood mononuclear cell and spleen cell cDNA libraries. IL-18Bpa is the most abundant of the 4 splice variants and is a putative member of the immunoglobulin superfamily. Its first 40 residues perfectly match the N-terminal sequence of urinary IL-18BP (see AAW8008). IL-18BP polypeptides capable of blocking IL-18 and/or modulating and/or blocking IL-18 activity are provided. Methods for their isolation and recombinant production, DNA vectors expressing them, vectors useful for their expression in humans and other mammals, and antibodies against them are also provided. IL-18BP polypeptides, and DNA encoding them, can be used to treat conditions requiring the protein (claimed). Conditions include autoimmune diseases, type I diabetes, rheumatoid arthritis, graft rejections, inflammatory bowel disease, sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain injury, chronic hepatitis, psoriasis, and chronic/facute pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX	Sequence	192 AA;		
XX	Query Match	100.0%; Score 164; DB 20; Length 192;		
XX	Best Local Similarity	100.0%; Pred. No. 6.1e-158;		
XX	Matches	164; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
OY	1	T P Y S Q T T A T A S Y R S T K P C P S O P P V F E R A K O C P A L E Y T W P E V E Y V P L G T L S L S C V A C S 60		
Db	29	t p v s q t t a t a s y r s t k p c p s o p p v f e r a k o c p a l e y t w p e v e y v p l g t l s l s c v a c s 88		
OY	61	R P P N F S I L Y W L G N G S F I E L P G R I W E G S S R E R G S T G T Q L K A V L Y E Q L T P A L H S T N F S C 120		
Db	89	r f p n f s i l y w l g n g s f i e l p g r i w e g s s r e r g s t g t q l k a v l e q i t p a l h s t n f s c 148		
OY	121	V L V D P E Q V V O R H V H V L A Q M A G L R A T L P P T Q E A L P S H S H S P Q Q G 164		
Db	149	v l v d p e q v v q r h v v l a q i w a g l r a t l p p t q e a l p s h s h s p q q g 192		
RESULT	3			
XX	ID	AY96292		
XX	AYY96292	standard; protein; 194 AA.		
AC	AYY96292;			
XX	DT	16-AUG-2000 (first entry)		
XX	DE	Human IGFAM-4 immunoglobulin.		
XX	HH	Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer; infection; inflammation; haematopoiesis; AIDS; allergy.		
XX	OS	Homo sapiens.		
XX	Key	Location/Qualifiers		
FT	Peptide	1..30		
FT	Protein	/label= signal_peptide 31..194 /label= IGFAM-4		
XX	PN	WO200029583-A2.		
PD		25-MAY-2000.		

XX  
 XX 19-NOV-1999; 99WO-US27566.  
 PR FT Key  
 PR FT Peptide 1..30  
 19-NOV-1998; 99US-0113635; /label= signal-peptide  
 22-DEC-1998; 98US-011635; 31-194  
 PR 07-APR-1999; 99US-0128194; FT Protein /label= "mature human IL-18 binding protein"  
 XX PN WO20012555-A1.  
 PA PN 09-MAR-2000.  
 (INCY-) INCYTE PHARM INC. PD 09-MAR-2000.  
 XX PI DR 01-SEP-1998; 98JP-0247588.  
 PI DR N-PSDB; AAA27384. PR 18-NOV-1998; 98JP-0327914.  
 XX PT Immunoglobulin superfamily proteins, the agonist and antagonist of the XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 PT protein is useful for preventing and treating disorders associated with PT PI Torige K, Tanai M, Kurimoto M;  
 PT altered levels of the protein such as cancer, immune system disorders XX DR N-PSDB; AAA11007.  
 PS Claim 1; Page 81; 105pp; English.  
 XX The present sequence is the human immunoglobulin superfamily protein  
 CC gene was isolated from a cDNA library of prostate tumour  
 CC tissue. It is expressed in nervous, haematopoietic and immune and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis,  
 CC arteriosclerosis, asthma, atherosclerosis, cholelithiasis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.  
 XX Sequence 194 AA;  
 SQ Query Match 100.0%; Score 164; DB 21; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 6.2E-158; Mismatches 0; Indels 0; Gaps 0;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPVSQTTAAATASVRASTKDPCCPSQPVPFRAAKQCQPALEYTWPEVEVPLNGTLSCLCVACS 60  
 Db 31 tpvsqtttaatasavristkdpccpsqpvpfraakqcqpaletwpevevplngtliscvacs 90  
 Qy 61 RFPNNSILWLGNSFIEHLGRMEGSTSRERSTGTCQICKALVLEQTPALISTNFSC 120  
 Db 91 rfpnsilwlgngsfiehlgrmegstsrerstgqickalvleqtpalhstnfsc 150  
 Qy 121 VLVDPEQVWQRHVLAQLWAGLRLATLPPQEAQSSHHSSPQQG 164  
 Db 151 vlvdpEqvqrhvlaqlwagrlratlppqeaqsshsppqqg 194  
 RESULT 4  
 AAY83985 ID AAY83985 standard; Protein; 194 AA.  
 AC XX  
 AC AAY83985; XX  
 AC AAW98006; XX  
 AC AAW98006; XX  
 DT 21-JUN-1999 (first entry)  
 DE Human interleukin-18 binding protein splice variant IL-18BPC.  
 XX Human interleukin-18 binding protein splice variant IL-18BPC.  
 KW Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant; XX  
 KW human; autoimmune disease; inflammation; diabetes; pancreatitis; XX  
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant; XX  
 KW autoimmune disease.  
 XX Homo sapiens.  
 XX OS Homo sapiens.

RESULT 6  
AY83982 ID AAY83982 standard; Protein; 137 AA..





ID AAY12716 standard; Protein; 55 AA.  
 XX  
 AC AAY12716;  
 XX DT 21-JUN-1999 (first entry)  
 XX DE Human 5' EST secreted protein SEQ ID NO:306.  
 XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haemopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; thrombolytic; anti-inflammatory; tumour inhibition.  
 XX OS Homo sapiens.  
 XX PN WO9906549-A2.  
 XX PD 11-FEB-1999.  
 XX PF 31-JUL-1998; 98WO-IB01231.  
 XX PR 01-AUG-1997; 97US-0905279.  
 XX PA (GEST ) GENSET.  
 XX PT Duclert A, Dumas Milne Edwards J, Lacroix B;  
 XX DR WPI: 1999-153779/13.  
 XX N-PSDB; AX51494.  
 XX PT New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from testis, ovary, uterus and spleen tissue  
 XX PS Claim 34; Page 404-405; 522PP; English.  
 XX : AX51459 to AX51691 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12681 to AAY12913, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, tissue growth regulating activity, reproductive hormone activity, tumour inhibition activity, haemopoiesis regulating activity, thrombolytic activity, chemotactic/chemokinetic activity, anti-inflammatory activity, receptor/ligand activity, or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.  
 XX Sequence 55 AA;  
 XX  
 Query Match 14.6%; Score 24; DB 20; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 AC QY 1 TPVSQTTAAATASVSRSTKDPCPSQ 24  
 DB 31 tpvsqttaaatasaqvstkdpcsq 54  
 XX SQ RESULT 13  
 ID AAYU3952  
 ID AAYU3952 standard; Protein; 165 AA.  
 XX AC AAYU3952;  
 XX DT 28-JUL-2000 (first entry)  
 DE Mouse mature interleukin 18 binding protein.  
 XX KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse; regulator; drug; sensitivity disease; organ rejection; organ transplant; autoimmune disease; rapid amplification of cDNA ends; RACE.  
 XX OS Mus musculus.  
 XX PN WO200012555-A1.  
 XX PD 09-MAR-2000.

---

DT 28-JUL-2000 (first entry)  
 XX DE Mouse IL-18 binding protein 5' RACE fragment #1 encoded protein.  
 XX KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse; regulator; drug; sensitivity disease; organ rejection; organ transplant; autoimmune disease; rapid amplification of cDNA ends; RACE.  
 XX OS Mus musculus.  
 XX PN WO200012555-A1.  
 XX PD 09-MAR-2000.  
 XX PR 18-NOV-1998; 98JP-0241588.  
 XX PR 18-NOV-1998; 98JP-0321914.  
 XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX PI Torigoe K, Tanai M, Kurimoto M;  
 XX DR WPI: 2000-237050/20.  
 DR N-PSDB; AAI11008.  
 XX PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
 XX PS Example 4; Page 65; 71PP; Japanese.  
 XX CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant, and in treating autoimmune diseases. This sequence represents the protein encoded by the initial fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends) reaction for the 5' end of the mouse interleukin 12 binding protein coding sequence.  
 XX SQ Sequence 117 AA;

XX  
PF 18-NOV-1998; 98WO-JP05186.  
XX  
PR 01-SEP-1998; 98JP-0247588.  
PR 18-NOV-1998; 98JP-0327914.  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Torigoe K, Taniai M, Kurimoto M;  
XX  
DR WPI; 2000-237850/20.  
DR N-PSDB; AAA11003.

XX  
PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
PT  
PR Example 4; Page 67-69; 71pp; Japanese.

XX  
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant, and in treating autoimmune diseases. This sequence represents the mature mouse interleukin 12 binding protein.  
CC  
SQ Sequence 165 AA;

XX  
CC Query Match 12.2%; Score 20; DB 21; Length 165;  
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
Ov 65 FSILYWLGNGSFTEHLPGRL 84  
AC ||||||| ||||| ||||| |||||  
Db 62 fsilywlgngsfiehlpgrl 81

RESULT 14  
AY83899 standard; Protein: 193 AA.  
XX  
AC AY83899;  
XX  
DT 28-JUL-2000 (first entry)  
DE Full length mouse interleukin 18 binding protein.  
XX  
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse; regulator; drug; sensitivity disease; organ rejection; organ transplant; autoimmune disease.  
XX  
OS Mus musculus.  
XX  
Key Location/Qualifiers  
FH 1..28  
FT /label= signal\_peptide  
FT 29..193  
FT /label= "nature IL-18 binding protein"  
XX  
PN WO200012555-A1.  
XX  
FT Peptide  
XX  
FT Protein  
XX  
FT /label= "nature IL-18 binding protein"  
XX  
PN 09-MAR-2000.  
XX  
PR 18-NOV-1998; 98WO-JP05186.  
PR 01-SEP-1998; 98JP-0247588.  
PR 18-NOV-1998; 98JP-0327914.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Torigoe K, Taniai M, Kurimoto M;  
XX  
DR WPI; 2000-237850/20.  
DR N-PSDB; AAA11005.

XX  
PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
PT  
PR Example 2; Page 61-62; 71pp; Japanese.

XX  
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant,

XX  
DR WPI; 2000-237850/20.  
DR N-PSDB; AAA11011.  
XX  
PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
PT  
PR Example 4; Page 67-69; 71pp; Japanese.

XX  
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant, and in treating autoimmune diseases. This sequence represents the full length mouse interleukin 12 binding protein.  
CC  
SQ Sequence 193 AA;

XX  
CC Query Match 12.2%; Score 20; DB 21; Length 193;  
CC Best Local Similarity 100.0%; Pred. No. 5e-12;  
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
Ov 65 FSILYWLGNGSFTEHLPGRL 84  
AC ||||||| ||||| ||||| |||||  
Db 90 fsilywlgngsfiehlpgrl 109

RESULT 15  
AY83983 standard; Protein: 49 AA.  
XX  
AC AY83983;  
XX  
DT 28-JUL-2000 (first entry)  
DE Human IL-18 binding protein N-terminus.  
XX  
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse; regulator; drug; sensitivity disease; organ rejection; organ transplant; autoimmune disease; rapid amplification of cDNA ends; RACE.  
XX  
OS Homo sapiens.  
XX  
PN WO200012555-A1.  
XX  
PD 09-MAR-2000.  
XX  
PR 18-NOV-1998; 98WO-JP05186.  
XX  
PR 01-SEP-1998; 98JP-0247588.  
PR 18-NOV-1998; 98JP-0327914.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Torigoe K, Taniai M, Kurimoto M;  
XX  
DR WPI; 2000-237850/20.  
DR N-PSDB; AAA11005.

XX  
PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -  
PT  
PR Example 2; Page 61-62; 71pp; Japanese.

XX  
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g. in slowing down rejection after organ transplant,

~ Wed Oct 9 15:32:08 2002

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Page 9

CC  
CC and in treating autoimmune diseases. This sequence represents the  
CC N-terminus of the interleukin 18 binding protein encoded by the 5' end  
CC of the gene isolated by a 5' RACE (Rapid Amplification of cDNA Ends)  
XX reaction.

SQ Sequence 49 AA:

Query Match 11.6%; Score 19; DB 21; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPVSQTTAATASVRSTKD 19  
||| ||| ||| ||| ||| |||  
Db 31 tpvsqttaatasvrstkd 49

Search completed: October 9, 2002, 01:52:26  
Job time: 5277 sec



OM protein - protein search, using sw model

Run on: October 9, 2002, 00:42:39 ; search time 61.98 Seconds  
(without alignments) 457.747 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 164

Sequence: 1 TPVSQTTAATASVRSKDP..... TLPPHQEALPSSHSSPQQG 164

Scoring table: ORIGO gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : STREMBL\_19;\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT 1 Q9UNH2 PRELIMINARY; PRT; 184 AA.  
ID Q9UNH2  
AC Q9UNH2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MC51L-53L-54L HOMOLOG (FRAGMENT).  
OS Homo sapiens (Human).  
OU Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SCIENCE FROM N.A.  
RX MEDLINE:99263157; PubMed=10329540;  
RA Xiang Y.; Moss B.;  
RT "Identification of human and mouse homologs of the MC51L-53L-54L family of secreted glycoproteins encoded by the *Molluscum* contagious poxvirus.";  
RT Virolgy 257:297-302(1999).  
RL EMBL; ARIB2908; AAD41053.1; -.  
DR InterPro; IPR03006; Ig\_MHC.  
DR Pfam; PF0047; Ig; 1.  
FT NON\_TER 184 AA; 19829 MW; F4B12D64BA6FD3A2 CRC64;  
SQ SEQUENCE

Query Match Best Local Similarity 100.0%; Score 164; DB 4; Length 184; Matches 164; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 TPVSQTTAATASVRSKDP..... TLPPHQEALPSSHSSPQQG 164

QY 1 TPVSQTTAATASVRSKDP..... TLPPHQEALPSSHSSPQQG 164

DB 21 TPVSQTTAATASVRSKDP..... TLPPHQEALPSSHSSPQQG 164

QY 61 RFPNSFLWLGNGSFIEHLPGGLWEGSTSRRERGSGTQLCKALVLFQTLPLAHNFSC 120

DB 81 RFPNSFLWLGNGSFIEHLPGGLWEGSTSRRERGSGTQLCKALVLFQTLPLAHNFSC 140

Q9YQD8 bacillus st  
Q9JIV3 rattus norv  
Q935Y1 streptococc  
Q91550 pseudomonas  
Q91X3 streptococc  
Q9maf4 drosophila  
Q97254 mycobacteri  
Q9V97 drosophila  
Q67396 aquifex aeo  
Q14882 homo sapien  
Q9yccl aeropyrum p  
Q9crs0 mus musculus  
Q9nk70 drosophila  
Q87694 chimpanzee  
Q9aln1 saecharopol  
Q9cs12 mus musculus  
Q9far4 streptomyce  
Q93m17 streptomyce  
Q9al10 streptococc  
Q9lbd2 brachydanio  
Q9yh60 brachydanio  
Q934u9 streptomyce  
Q9hax3 homo sapien  
Q9hax2 homo sapien  
Q9ibr4 bacillus ha  
Q9tbq3 bacillus st  
Q9tqg9 arrobiodopsis  
Q9c101 schizosacch

Result No. Score Match Length DB ID Description

1 164 100.0 184 4 Q9UNH2

2 164 100.0 194 4 Q9UBR7

3 97 59.1 161 4 Q9NZQ9

4 27 16.5 193 11 Q9JLN2

5 20 12.2 192 11 Q9Z0N9

6 19 11.6 218 12 Q9TM13

7 19 11.6 235 12 Q98222

8 15 9.1 99 11 Q9CV30

9 11 8 4.9 290 3 Q9USK4

10 11 8 4.9 421 4 Q15329

11 11 8 4.9 467 10 Q04127

12 11 8 4.9 505 10 Q04129

13 11 8 4.9 634 5 Q9VQD2

14 11 8 4.9 647 5 Q96613

15 8 4.9 647 5 Q96613

16 8 4.9 647 5 Q96613

RESULT . 2				
ID 09UBR7	PRELIMINARY;	PRT; 194 AA.		
AC 09UBR7;				
DT 01-MAY-2000 (TREMBlrel. 13, Created)				
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)				
DE INTERLEUKIN 18 BINDING PROTEIN PRECURSOR.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX NCBI_TAXID=9606;				
RP SEQUENCE FROM N.A.				
RC TISSUE=LIVER;				
RX PMID=99192308; PubMed=10094485;				
RA Aizawa Y., Akita K., Tanai M., Korigoe K., Mori T., Nishida Y.'				
RA Ushio S., Nakada Y., Tamimoto T., Ikegami H., Ikeda M., Kurimoto M.;				
RT "Cloning and expression of interleukin-18 binding protein.";				
RL FEBS Lett. 445:358-342(1999).				
RN [2]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=9923157; PubMed=10329540;				
RA Xiang Y., Moss B.;				
RT "Identification of human and mouse homologs of the <i>Molluscum contagiosum</i> family of secreted glycoproteins encoded by the <i>Molluscum contagiosum</i> poxvirus."; Virology 257:297-302(1999).				
RL EMBL; AB019504; BAA7674.1; -.				
DR EMBL; AF122506; ARD41051.1; -.				
DR InterPro; IPR003006; Ig-MHC.				
DR Pfam; PF00047; ig_1.				
KW Signal.				
FT SIGNAL_1 1 30 POTENTIAL.				
FT CHAIN_3 1 194 AA; 21099 MW; 5E520D646AF8A3 CRC64;				
SQ				
Query Match 100.0%; Score 164; DB 4; Length 194; Best Local Similarity 100.0%; Pred. No. 1.3e-159; Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 TPVSQTATATASVRSKTPCPQSOPPVPAKQCPALETWTPEEVPLNGTLSSLSCVACS 60				
Db 31 TPVSQTATATASVRSKTPCPQSOPPVPAKQCPALETWTPEEVPLNGTLSSLSCVACS 90				
QY 61 RPPNFSILWLGNGSFIEHLPGRLWEGSTSRRGSGTGTOLCKALVLEQIPTPALISTNFSC 120				
Db 91 RPPNFSILWLGNGSFIEHLPGRLWEGSTSRRGSGTGTOLCKALVLEQIPTPALISTNFSC 150				
QY 121 VLPDPEQWVQRHVLAQWAGLATLPPIQEAAPSSHSQQQG 164				
Db 151 VLVDPEQWVQRHVLAQWAGLRTLPPIQEAALPSSHSQQQG 194				
RESULT . 3				
ID 09NZA9	PRELIMINARY;	PRT; 161 AA.		
AC 09NZA9;				
DT 01-OCT-2000 (TREMBlrel. 15, Created)				
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)				
DE INTERLEUKIN-18 BINDING PROTEIN D.				
GN IL18BP.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OC NCBI_TAXID=9606;				
*NCBI_TAXID=9606;				
RESULT . 4				
ID 09JLN2	PRELIMINARY;	PRT; 193 AA.		
AC 09JLN2;				
DT 01-OCT-2000 (TREMBlrel. 15, Created)				
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)				
DE INTERLRUKIN 18 BINDING PROTEIN.				
GN IL18BP.				
OS Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciuromorphati; Muridae; Murinae; Rattus.				
OX NCBI_TAXID=10116;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=LEWIS;				
RT Im S.H., Venkatesh N., Barchan D., Souroujon M.C., Fuchs S.;				
RT "Cloning and characterization of rat IL-18 binding protein.";				
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
DR AF154599; AAH72102.1; -.				
SQ SEQUENCE 193 AA; 21085 MW; BDB23D80E44B44B0 CRC64;				
Query Match 16.5%; Score 11; DB 11; Length 193; Best Local Similarity 100.0%; Pred. No. 1.9e-19; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 58 ACCSRPNFSILWLGNGSFIEHLPGRL 84				
Db 83 ACCSRPNFSILWLGNGSFIEHLPGRL 109				
RESULT . 5				
ID 09Z0M9	PRELIMINARY;	PRT; 191 AA.		
AC 09Z0M9;				
DT 01-MAY-1999 (TREMBlrel. 10, Created)				
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)				
DE INTERLEUKIN-18 BINDING PROTEIN D PRECURSOR.				
GN IGFBP OR IL18BP.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciuromorphati; Muridae; Murinae; Mus.				
OX NCBI_TAXID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=99146382; PubMed=10023777;				



DT	01-OCT-2000 (TREMBrel. 15, Created)	DT	01-JUN-2001 (TREMBrel. 17, Created)
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	DT	01-JUN-2001 (TREMBrel. 17, Last sequence update)
DE	INTERLEUKIN 18 BINDING PROTEIN.	DE	INTERFERON GAMMA INDUCING FACTOR BINDING PROTEIN (FRAGMENT).
GN	054L.	GN	IGIFB.
OS	Molluscum contagiosum virus subtype 1 (MCV1).	OS	Mus musculus (Mouse).
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Molluscipoxvirus.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10280;	OX	NCBI_TaxID=10090;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAT="MADRID 99;"	RC	STRAT=C57BL/6J; TISSUE=TONGUE;
RX	MEDLINE=20031932; PubMed=10769064;	RX	MEDLINE=2108560; PubMed=11217851;
RA	Smith V.P., Bryant N.A., Alcamo A.;	RA	Kawai J., Shingara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RT	"Ectromelia, vaccinia and camelpox viruses encode secreted interleukin 18 binding proteins";	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RL	J. Gen. Virol. 81:1223-1230(2000).	RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
DR	EMBL: AJ271163; CAB38141; -.	RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
SQ	SEQUENCE 218 AA; 3FFA9C240DD24E75 CRC64;	RA	Kadota K., Matsuda H.A., Ashburner M., Battalio S., Casavant T.,
RESULT 9	Query Match 11.6%; Score 19; DB 12; Length 218; Best Local Similarity 100.0%; Pred. No. 3.3e-11; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Rodriguez T., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Haseeda Y., Kawaji H., Rohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
098222	PRELIMINARY; PRT; 235 AA.	RT	DR
ID	Q98222	DR	MGI; MGI:1333800; Ig1fbp.
AC	098222	FT	NON_TER 1 1
Db	114 HSTNFSCVLVDPEQVWQRH 132	SQ	SEQUENCE 99 AA; 10869 MW; 2CB0B739D5DABEB CRC64;
DT	01-FEB-1997 (TREMBrel. 02, Created)	RESULT 9	Query Match 9.1%; Score 15; DB 11; Length 99; Best Local Similarity 100.0%; Pred. No. 1.9e-07; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-FEB-1997 (TREMBrel. 02, Last sequence update)	098222	RT
DT	01-NOV-1998 (TREMBrel. 08, Last annotation update)	AC	098222
DE	MC054L.	AC	098222
GN	MC054L.	AC	098222
OS	Molluscum contagiosum virus subtype 1 (MCV1).	AC	098222
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	AC	098222
OC	Molluscipoxvirus.	AC	098222
OX	[1]	AC	098222
RN	SEQUENCE FROM N.A.	AC	098222
RP	SEQUENCE FROM N.A.	AC	098222
RX	MEDLINE=96325459; PubMed=8670425;	AC	098222
RA	Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;	AC	098222
RA	"Genome sequence of a human tumorigenic poxvirus: Prediction of specific host response-evasion genes.>"; Science 273:813-816(1996).	AC	098222
RT	[2]	AC	098222
RL	SEQUENCE FROM N.A.	AC	098222
RN	SEQUENCE FROM N.A.	AC	098222
RA	Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;	AC	098222
RA	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.	AC	098222
DR	EMBL: U60315; AAC55182.1; -.	AC	098222
SQ	SEQUENCE 235 AA; 125209 MW; BA47745CC68608889 CRC64;	AC	098222
RESULT 9	Query Match 11.6%; Score 19; DB 12; Length 235; Best Local Similarity 100.0%; Pred. No. 3.5e-11; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	098222	PRELIMINARY; PRT; 290 AA.
OY	114 HSTNFSCVLVDPEQVWQRH 132	098222	PRELIMINARY; PRT; 290 AA.
Db	113 HSTNFSCVLVDPEQVWQRH 131	098222	PRELIMINARY; PRT; 290 AA.
RESULT 10	Query Match 4.9%; Score 8; DB 3; Length 290; Best Local Similarity 100.0%; Pred. No. 3.5e-11; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	09CV30	PRELIMINARY; PRT; 99 AA.
ID	09CV30	09CV30	PRELIMINARY; PRT; 99 AA.
AC	09CV30	09CV30	PRELIMINARY; PRT; 99 AA.

Qy	148	PTQEALPS	155		Best Local Similarity 100.0%; Pred. No. 7.6; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	235	PTQEALPS	242		
RESULT	12				
O15329		PRELIMINARY;	PRT;	421 AA.	
ID	O15329				
AC	O15329;				
DT	01-JAN-1998	(TREMBLrel. 05, Created)			
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)			
DE	1-DCC-2001 (TREMBLrel. 19, Last annotation update)				
GN	SECRETORY MUCIN MUC6 (FRAGMENT).				
MU6.					
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-9319895; PubMed=7600650;				
RA	Toribara N.W., Robertson A.M., Ho S.B., Kuo W.L., Gum E., Hicks J.W.,				
RA	Gum J.R. Jr., Byrd J.C., Sidiki B., Kim Y.S.;				
RT	"Human gastric mucin. Identification of a unique species by expression cloning.";				
RT	J. Biol. Chem. 268:5879-5885(1993).				
RL	[2]				
RN	SEQUENCE FROM N.A. PubMed=9195947;				
RX	MEDLINE-97341178; PubMed=9195947;				
RA	Toribara N.W., Ho S.B., Gum E., Gum J.R. Jr., Lau P., Kim Y.S.;				
RT	"The carboxyl-terminal sequence of the human secretory mucin, MUC6.				
RT	Analyses of the primary amino acid sequence.";				
RL	J. Biol. Chem. 272:16398-16403(1997).				
DR	EMBL; U77698; AAC51370_1; -				
DR	InterPro; IPR00355; Cys_knot.				
DR	Pfam; PF00007; CYS_knot; 1.				
DR	SMART; SM00041; CYS_1.				
DR	PROSITE; PS01225; CTCK_2; 1.				
FT	NON_TER 1 1.				
SEQUENCE	421 AA; 4217 MW; 90E319ED223A9F80 CRC64;				
Query Match	4.9%; Score 8; DB 4; Length 421;				
Best Local Similarity 100.0%; Pred. No. 11;					
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	154	PSHSSPQ	161		
Db	128	PSHSSPQ	135		
RESULT	13				
O04127		PRELIMINARY;	PRT;	467 AA.	
ID	O04127;				
AC	O04127;				
DT	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)				
DE	LETAL LEAF-SPO1 (FRAGMENT).				
GN	LSSL.				
OS	Zea mays (Maize)				
OC	Bukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Moniliophytina; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; zea.				
OC	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
Qy	148	PTQEALPS	155		
Db	422	PTQEALPS	429		
RESULT	13				
O04127		PRELIMINARY;	PRT;	467 AA.	
ID	O04127;				
AC	O04127;				
DT	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)				
DE	LETAL LEAF-SPO1 (FRAGMENT).				
GN	LSSL.				
OS	Zea mays (Maize)				
OC	Bukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Moniliophytina; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; zea.				
OC	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
Qy	148	PTQEALPS	155		
Db	422	PTQEALPS	429		
RESULT	15				
O9VDD2		PRELIMINARY;	PRT;	634 AA.	
ID	O9VDD2				
AC	O9VDD2;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	SNF4AGAMMA PROTEIN.				
GN	SNF4AGAMMA OR SNF4AGAMMA OR CG17299.				
OS	Drosophila melanogaster (Fruit fly)				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Neciptera; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriodea; Drosophilidae; Drosophila.				
OC	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abril J.F., Abyzov A., An H.-J., Andrews-Pflanck C., Baldwin D.,  
 Balow R.M., Basu P., Baxendale J., Barakatoglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 Borkova D., Botchan M.R., Bock J., Brokstein P., Brottier P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibebewam C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J.A., Li J.Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy E., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacileb J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stappleton M., Strong R., Sun E.,  
 Svistkis R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Ra Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 Science 287: 2185-2195 (2000).  
 DR EMBL: AE003733; AA055864..1..;  
 DR Flybase; FBgn0025803; SNF4A-gamma.  
 DR InterPro; IPR000644; CBS.  
 DR Pfam; PF00571; CBS; 4.  
 DR SMART; SM00116; CBS; 4.  
 DR SEQUENCE 634 AA; 70174 MW; 3FFD0D53E54BBE7C CRC64;

Query Match Score 8; DB 5; Length 634;  
 Best Local Similarity 4.9%; Score 8; DB 5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	5	QTPRATA	12
Db	544	QTPRATA	551

Search completed: October 9, 2002, 01:53:45  
 Job time: 4265 sec





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RN	(1)
RP	SEQUENCE FROM N.A.
RC	
TISSUE=Brain;	
RX	MEDLINE=98226558; PubMed=9566905;
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;
RA	"Axil, a member of the Axin family, interacts with both glycoprotein synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos."
RT	Mol. Cell. Biol. 18:2867-2875(1998).
RL	-!!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC	-!!- SUBUNIT: INTERACTS WITH GLYCOPROTEIN KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC	-!!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC	-!!- PTM: PROBABLY PHOSPHORYLATED BY PP2A.
CC	-!!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC	-!!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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CC	EMBL; AF017757; AAC40089.1; -.
DR	HSSP; P4999; IAGR.
DR	InterPro; IPR00158; DIX.
DR	InterPro; IPR000342; RGS.
DR	Pfam; PF00778; DIX; 1.
DR	Pfam; PF00615; RGS; 1.
DR	ProDom; PDO01580; RGS; 1.
DR	ProDom; PDO03339; DIX; 1.
DR	SMART; SM00021; DAX; 1.
DR	SMART; SM00315; RGS; 1.
DR	PROSITE; BS50132; RGS; 1.
KW	Developmental protein; Phosphorylation.
FT	DOMAIN 81 200 RGS.
FT	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT	DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT	POLY-HIS.
FT	DOMAIN 469 474 POLY-HIS.
FT	SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;
Query Match	4.9%; Score 8; DB 1; Length 443;
Best Local Similarity	100.0%; Pred. No. 2;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	106 LEQLTPAL 113
Db	41 LEQLTPAL 48
RESULT 4	
ID	AXN2_RAT STANDARD; PRT; 838 AA.
ID	070240; 16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-Oct-2001 (Rel. 40, Last annotation update)
DE	Axin 2 (Axis inhibition protein 2) (Conductin) (Axin-like protein)
DE	(Axin1).
GN	AXIN2.
OS	Rattus norvegicus (Rat).
OC	Mammalia; Eutheria; Rodentia; Sciurognathini; Muridae; Murinae; Rattus.
AXN2_RAT	
RESULT 5	
ID	AXN2_MOUSE STANDARD; PRT; 840 AA.
ID	088366; Q9QXJ6; 16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-Oct-2001 (Rel. 40, Last annotation update)
DE	Axin 2 (Axis inhibition protein 2) (Conductin) (Axin-like protein)
DE	(Axin1).
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	

Query Match 4.9%; Score 8; DB 1; Length 840;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

DR SMART; SM0021; DAX; 1.  
DR SMART; SM00315; RGS; 1.  
DR PROS1; PS50132; RGS; 1.  
KW Developmental protein; Phosphorylation.

Query Match 4.9%; Score 8; DB 1; Length 843;  
 Best Local Similarity 100.0%; Pred. No. 3.6; Length 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATASVRT 17  
 Db 257 ATASVRT 264

RESULT 7

IOVO\_CIRAE STANDARD; PRT; 54 AA.

ID IOVO\_CIRAE STANDARD; PRT; 54 AA.

AC P05579; DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, last sequence update)

DT 01-MAR-2002 (Rel. 41, last annotation update)

DE Ovomucoid (Fragment).

OS Circus aeruginosus (Marsh harrier).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Falconiformes; Accipitridae; Accipitrinae; Circus.

OC NCBI\_TAXID=8964;

RN [1]

RP SEQUENCE.

RX MEDLINE=87157615; PUBMED=3828298;

RX MEDLINE=93020000; PUBMED=4465833;

RA Laskowski M. Jr., Kato I., Ardel W., Cook J., Denton A., Empie M.W., Kohr W.J., Park S.J., Parks K., Schatzley B.L., Schoenberger O.L., Tashiro M., Vichot G., Whately H.E., Wieczorek A., Wieczorek M.; RT "Ovomucoid third domains from 100 avian species: isolation, sequences, and hypervariability of enzyme-inhibitor contact residues"; RL Biochemistry 26:202-221(1987).

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- FAMILY INHIBITORY DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

DR HSSP; P05586; 4OVO; InterPro; IPR02350; kazal.

DR Pfam; PF0050; kazal; 1.

DR SMART; SM00280; KAZAL; 1.

DR PROSITE; PS00282; KAZAL; 1.

DR NON\_TER FT Serine protease inhibitor; Glycoprotein; Repeat; Egg white.

DR SMART; SM00280; KAZAL; 1.

DR PROSITE; PS00282; KAZAL; 1.

KW Serine protease inhibitor; Glycoprotein; Repeat; Egg white.

FT DOMAIN 81 200 RGS.  
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).  
 FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY SIMILARITY).

FT DOMAIN 469 474 POLY-HIS.

FT DOMAIN 761 843 DIX.

FT CONFLICT 37 62 QPGVKGQQTKPMSSVSSNTRRNEDGL -> HHGGGPGHQT HVCLIQHQQRWV (IN REF. 2).  
 FT CONFLICT 346 346 Q -> R (IN REF. 2).  
 FT CONFLICT 572 636 MISSING (IN REF. 2).  
 FT CONFLICT 687 687 P -> S (IN REF. 2).  
 FT CONFLICT 696 696 Q -> H (IN REF. 2).

SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6AB4664D CRC64;

Query Match 4.9%; Score 8; DB 1; Length 843;  
 Best Local Similarity 100.0%; Pred. No. 3.6; Length 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NGTISLS 55  
 Db 43 NGTISLS 49

RESULT 8

IOVO\_OPIHO STANDARD; PRT; 54 AA.

ID IOVO\_OPIHO STANDARD; PRT; 54 AA.

AC P52349; DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Ovomucoid (Fragment).

OS Opisthothecum hoazin (Hoatzin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Opisthothecumidae; Opisthothecum.

OC NCBI\_TAXID=30419;

RN [1]

RP SEQUENCE.

RX MEDLINE=94072078; PUBMED=8251062;

RX Apostol I., Gileatto A., Komiyama T., Zhang W., Laskowski M. Jr.; RT "Amino acid sequences of ovomucoid third domains from 27 additional species of birds".  
 RL J. Protein Chem. 12:419-433(1993);  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: AVIAN OVOMUCOID CONSIST OF THREE HOMOLOGOUS, TANDEM KAZAL FAMILY INHIBITORY DOMAINS.

CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

DR HSSP; P05586; 4OVO; InterPro; IPR02350; kazal.

DR Pfam; PF0050; kazal; 1.

DR SMART; SM00280; KAZAL; 1.

DR PROSITE; PS00282; KAZAL; 1.

DR KW Serine protease inhibitor; Glycoprotein; Repeat; Egg white.

FT DOMAIN 4 54 KAZAL-LIKE 3.  
 FT ACT\_SITE 16 17 REACTIVE BOND 3.

FT DISULFID 6 36

FT DISULFID 14 33

FT DISULFID 22 54

FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).

FT NON\_TER 54 54

FT SEQUENCE 54 AA; 5828 MW; 95B10804D446583D CRC64;

Query Match 4.3%; Score 7; DB 1; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 3.2; Length 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NGTISLS 55  
 Db 43 NGTISLS 49

RESULT 9

PER\_DROAN PER\_DROAN STANDARD; PRT; 125 AA.

ID PER\_DROAN STANDARD; PRT; 125 AA.

AC P03393; DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Period circadian protein (Fragment).

GN PER.

OS Drosophila ananassae (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydriidae; Drosophilidae; Drosophila.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9319682; PUBMED=8450754;

RA Peikoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;





DR	Pfam; PF02801; ketocycl-synt_C; 1.	CC	-!- FUNCTION: CATALYZES THE ISOMERIZATION OF PROSTAGLANDIN H2 TO PROSTACYCLIN (=> PROSTAGLANDIN 12).
KW	Antibiotic biosynthesis; Transferase; Acyltransferase.	CC	-!- CATALYTIC ACTIVITY: (52,13E)-(11S)-9-alpha,11-alpha-epidioxy-15-hydroxyprosta-5,13-dienoate => (52,13E)-(11S)-6,9-alpha-epoxy-11-alpha,15-dihydroxyprosta-5,13-dienoate.
SEQUENCE	402 AA;	CC	-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE. MAY BE ANCHORED TO THE MEMBRANE VIA A SINGLE TRANSMEMBRANE DOMAIN.
SO	41270 MW;	CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED; PARTICULARLY ABUNDANT IN OVARY, HEART, SKELETAL MUSCLE, LUNG, AND PROSTATE.
Query Match	Best Local Similarity 4.3%; Score 7; DB 1; Length 402; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
Qy	78 EHLPGRL 84	CC	-!- DATABASE: NAME-Cytochrome P450 Allele Nomenclature Committee; NOTE=CYP8A1 alleles; WWW="http://www.umm.ki.se/cypalleles/cyp8a1.htm".
Db	59 EHLPGRL 65	CC	CC
RESULT 14		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi-sib.ch/announce-or-send-an-email-to-license@ebi-sib.ch">http://www.ebi-sib.ch/announce-or-send-an-email-to-license@ebi-sib.ch</a> ).
PTG1_HUMAN	STANDARD; PRT; 500 AA.	CC	CC
ID	PTG1_HUMAN	CC	ANCHORED TO THE MEMBRANE VIA A SINGLE TRANSMEMBRANE DOMAIN.
AC	011667; DT 01-NOV-1997 (Rel. 35, Created)	CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED; PARTICULARLY ABUNDANT IN OVARY, HEART, SKELETAL MUSCLE, LUNG, AND PROSTATE.
DT	01-NOV-1997 (Rel. 35, Last sequence update)	CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DT	01-MAR-2002 (Rel. 41, Last annotation update)	CC	-!- DATABASE: NAME-Cytochrome P450 Allele Nomenclature Committee; NOTE=CYP8A1 alleles; WWW="http://www.umm.ki.se/cypalleles/cyp8a1.htm".
DE	Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin I2 synthase).	CC	CC
GN	PTGIS OR CYP8B OR CYTB8A1.	CC	CC
OS	Homo sapiens (Human).	CC	CC
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	CC	CC
OX	NCBI_TAXID=9606;	CC	CC
RN	[1]	CC	CC
SEQUENCE FROM N.A.		CC	CC
RC		CC	CC
RX	TISSUE=Aorta; MEDLINE=99242006; PubMed=818632;	CC	CC
RA	Miyata A., Hara S., Yokoyama C., Inoue H., Ulrich V., Tanabe T.; "Molecular cloning and expression of human prostacyclin synthase.", Biochem. Biophys. Res. Commun. 200:1728-1734(1994).	CC	CC
RL	[2]	CC	CC
RP	SEQUENCE FROM N.A.' AND VARIANTS LEU-38; ARG-118 AND SER-379.	CC	CC
RX	MEDLINE=21177061; PubMed=11281454;	CC	CC
RA	Chevalier J.C., Cauffiez C., Bernard C., Lo-Guidice J.-M., Allorge D., Fazio F., Ferrari N., Libera C., Lhermitte M., D'Halluin J.C., Broly F.; "Characterization of new mutations in the coding sequence and 5'-untranslated region of the human prostacyclin synthase gene (CYP8A1)."; Hum. Genet. 108:148-155(2001).	CC	CC
RN	[3]	CC	CC
RP	SEQUENCE FROM N.A.	CC	CC
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beale D.M., Beasley O.P., Bird C.P., Blahey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W., Butler A.P., Carter C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleef C.M., Clegg S., Cobley V.E., Collier R., Connor N.R., Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimber A.M., King A., Knights A., Laird G.K., Lawlor S., Lehraslahti M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D., Marsh S.L., Martin S.L., McCannagh L.J., McLay K., McMurray A.A., Milne S., Mistri D., Moore M.J., Mullican J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E., Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J., RT	CC	CC
BL	"The DNA sequence and comparative analysis of human chromosome 20.", Nature 414:865-871(2001).	CC	CC
Query Match	Best Local Similarity 4.3%; Score 7; DB 1; Length 500; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	-!- FUNCTION: CATALYZES THE ISOMERIZATION OF PROSTAGLANDIN H2 TO PROSTACYCLIN (=> PROSTAGLANDIN 12).
Qy	2 PVSQRTT 8	CC	-!- CATALYTIC ACTIVITY: (52,13E)-(11S)-9-alpha,11-alpha-epidioxy-15-hydroxyprosta-5,13-dienoate => (52,13E)-(11S)-6,9-alpha-epoxy-11-alpha,15-dihydroxyprosta-5,13-dienoate.
Db	323 PVSQRTT 329	CC	-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE. MAY BE ANCHORED TO THE MEMBRANE VIA A SINGLE TRANSMEMBRANE DOMAIN.
RESULT 15		CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED; PARTICULARLY ABUNDANT IN OVARY, HEART, SKELETAL MUSCLE, LUNG, AND PROSTATE.
EFG1_CANAL	STANDARD; PRT; 552 AA.	CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
ID	EFG1_CANAL	CC	-!- DATABASE: NAME-Cytochrome P450 Allele Nomenclature Committee; NOTE=CYP8A1 alleles; WWW="http://www.umm.ki.se/cypalleles/cyp8a1.htm".
AC	P43064; DT 01-NOV-1995 (Rel. 32, Created)	CC	CC
DT	01-NOV-1995 (Rel. 32, Last sequence update)	CC	CC
DT	30-MAY-2000 (Rel. 39, Last annotation update)	CC	CC
DE	Enhanced filamentous growth protein.	CC	CC
GN	EFG1 OR EFG.	CC	CC
OS	Candida albicans (yeast).	CC	CC
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetes; mitosporic Saccharomycetales; Candida.	CC	CC
OX	NCBL_TAXID=5476;	CC	CC
RN	[1]	CC	CC
RP	SEQUENCE FROM N.A.	CC	CC
RC	STRAIN=ATCC 10231;	CC	CC
RX	MEDLINE=97299575; PubMed=1955024;	CC	CC
RA	Stoldt V.R., Sonnenburg A., Leuker C.E., Ernst J.F.; "Efg1p, an essential regulator of morphogenesis of the human pathogen Candida albicans, is a member of a conserved class of bHLH proteins	CC	CC

RT regulating morphogenetic processes in fungi.";  
 RL EMBO J. 16:1982-1991(1997).  
 CC -!- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT STIMULATES  
 CC PSEUDOHYPHAL MORPHOGENESIS.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE EFG1/PHD/STU1 FAMILY.  
 CC  
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 CC  
 DR EMBL; Z32687; CAA83640.1; -.  
 DR InterPro; IPR003163; Yeast\_DNA\_bind.  
 DR Pfam; PF02292; Yeast\_DNA\_bind\_1.  
 KW Transcription regulation; Nuclear protein; DNA-binding.  
 FT DOMAIN 34 37 POLY-GLN.  
 FT DOMAIN 45 50 POLY-GLN.  
 FT DOMAIN 83 93 POLY-GLN.  
 FT DOMAIN 315 326 POLY-ALA.  
 FT DOMAIN 332 338 POLY-PRO.  
 FT DOMAIN 438 446 POLY-GLN.  
 FT DOMAIN 470 473 POLY-GLN.  
 FT DOMAIN 483 493 POLY-GLN.  
 FT DOMAIN 496 499 POLY-GLN.  
 SQ SEQUENCE 552 AA; 59964 MW; F94FD94FC2E06BB7 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 552;  
 Best Local Similarity 100.0%; Pred No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 TTTAATA 12  
 |||||  
 Db 343 TTTAATA 349

Search completed: October 9, 2002, 02:52:57  
 Job time: 3938 sec



OM protein - protein search, using sw model

Run on: October 9, 2002, 00:57:49 ; Search time 38.03 Seconds  
 (without alignments)  
 414.374 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 164

Sequence: 1 TPVSOTTAAATASVRSTKDP..... TLPPPIQEALPSSHSSPQQQG 164

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 7.1:  
 1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	19	11.6	T30656	hypothetical protein 54L - Molluscum contagiosum virus 1
2	8	4.9	T50434	N;Alternate names: MC054L
3	8	4.9	S74377	C;Species: Molluscum contagiosum virus 1
4	8	4.9	E64725	C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
5	8	4.9	H90634	C;Accession: T30656
6	8	4.9	H85485	R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
7	8	4.9	T04136	A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
8	8	4.9	T08423	A;Reference number: 220876; MUID:96325459
9	7	4.3	B31443	A;Accession: T30656
10	7	4.3	H61588	A;Status: preliminary; translated from GB/EMBL/DDJB
11	7	4.3	T49624	A;Molecule type: DNA
12	7	4.3	F83531	A;Residues: 1-235 <SEN>
13	7	4.3	C70527	A;Cross-references: EMBL:AL132870; PIDN:CAR60688.1; GSPDB:GN00068; SPDB:SPCC4B3.14
14	7	4.3	A70421	A;Experimental source: strain 972h(-); cosmid c4B3
15	7	4.3	S37595	A;Genetics:
16	7	4.3	A72609	A;Gene: SPDB:SPCC4B3.14
17	7	4.3	C54258	A;Status: preliminary; translated from GB/EMBL/DDJB
18	7	4.3	S35090	A;Molecule type: DNA
19	7	4.3	S25077	A;Residues: 1-290 <SEE>
20	7	4.3	JC2231	A;Cross-references: EMBL:AL132870; PIDN:CAR60688.1; GSPDB:GN00068; SPDB:SPCC4B3.14
21	7	4.3	E83882	A;Experimental source: strain 972h(-); cosmid c4B3
22	7	4.3	M51	A;Genetics:
23	7	4.3	S49338	A;Gene: SPDB:SPCC4B3.14
24	7	4.3	D97431	A;Map position: 3
25	7	4.3	T46880	Query Match
26	7	4.3	D97676	Best Local Similarity 4.9%; Score 8; DB 2; Length 290;
27	7	4.3	613	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28	7	4.3	AB2901	ATP-dependent heli
29	7	4.3	630	2 AD3272
2	7	4.3	702	A69140

Qy 148 PTQEALPS 155  
 Db |||||  
 235 PTQEALPS 242

RESULT 3  
 S74377 riboflavin bifunctional biosynthesis protein ribG [similarity] - Synechocystis sp. (strain N; Alternate names: hypothetical protein srl0066; riboflavin-specific deaminase  
 N; Contains: 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193); diaminohyd C; Species: Synechocystis sp.

A; Variety: PCC 6803  
 C; Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
 C; Accession: S74377  
 R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996  
 A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.  
 A; Reference number: S74322; MUID: 97061201  
 A; Accession: S74377  
 A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-368 <RAN>  
 A; Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10295\_1; PID:g100115  
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C; Genetics: A; Gene: ribG  
 C; Superfamily: Chlamydophila pneumoniae riboflavin-specific deaminase  
 C; Keywords: hydrolase; oxidoreductase

Query Match 4.9%; Score 8; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 LVLEQLTP 111  
 Db 254 LVLEQLTP 271

RESULT 4  
 E64725 yaau protein - Escherichia coli  
 C; Species: Escherichia coli  
 C; Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 20-Jun-2000  
 C; Accession: E64725; S40566  
 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A; Rose, D.J.; Mau, B.; Shao, Y.; Science 277, 1453-1462, 1997  
 A; Title: The complete genome sequence of Escherichia coli K-12.  
 A; Reference number: A64720; MUID: 97426617  
 A; Accession: E64725  
 A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-443 <BLAT>  
 A; Cross-references: GB:BAE00014; GB:U00096; NID:g1786217; PIDN: AAC73156.1; PID:g1786229; A; Experimental source: strain K-12, substrain MG1655 R; Yura, T.; Mori, H.; Naiji, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isano, K.; Mizobu submitted to the EMBL Data Library, December 1992 A; Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2 A; Reference number: S40531  
 A; Accession: S40566  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: MNSRSKKG' 233-239; 'C' 241-303; 'S' 305-394; 'D' 396-443 <YUR> A; Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01321.1; PID:g216470  
 C; Genetics: A; Gene: yaau  
 A; Superfamily: yaau protein  
 C; Keywords: transmembrane protein; transport protein  
 F; 2541/Domain: transmembrane #status predicted <TM1>

Query Match 4.9%; Score 8; DB 2; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 LEQFLPAL 113  
 Db 41 LEQFLPAL 48

RESULT 5  
 H90634 probable transport protein EC50048 [imported] - Escherichia coli (strain Q157:H7, sub A; Accession: H90634  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-443 <HAY>  
 A; Cross-references: GB:BA00007; PIDN: BAB33471.1; PID:g13359504; GSPDB:GN01154  
 A; Experimental source: strain 0157:H7, substrain RIMD 0509952  
 C; Genetics:  
 A; Gene: EC50048  
 C; Superfamily: yaau protein

Query Match 4.9%; Score 8; DB 2; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 LEQFLPAL 113  
 Db 41 LEQFLPAL 48

RESULT 6  
 H85485 probable transport protein yaau [imported] - Escherichia coli (strain 0157:H7, substr C; Species: Escherichia coli  
 C; Date: 15-Feb-2001 #sequence\_revision 15-Feb-2001 #text\_change 14-Sep-2001  
 C; Accession: H85485  
 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.; Potamitis, K.; Apod Nature 409, 529-533, 2001  
 A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.  
 A; Reference number: A85480; MUID: 21074935; PMID:11206551  
 A; Accession: H85485  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-443 <TPO>  
 A; Cross-references: GB:AB005174; NID:g12512735; PIDN:AAG54348.1; GSPDB:GN00115; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933  
 C; Genetics:  
 A; Gene: yaau  
 C; Superfamily: yaau protein

	Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Query Match	4.9%	; Score 8; DB 2;	Length 443;							
Best Local Similarity	100.0%	; Pred. No. 4.4;								
Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	106 LSQLTPAL 113									
Db	41 LEQLTPAL 48									
RESULT	7									
T04136	Cell death suppressor protein l1sl - maize	B31443	ovomucoid, third domain - western marsh harrier (fragment)	C;Species: Circus aeruginosus (western marsh harrier)	C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Feb-1997					
N;Alternate names: lethal leaf-spot 1	C;Accession: B31443	R;Laskowski Jr., M.; Kato, I.; Ardel, W.; Cook, J.; Denton, A.; Empie, M.W.; Kohr, W.								
C;Species: Zea mays (maize)	C;Accession: T04136; T04133	, A.; Wieczorek, M.; Biochemistry 26, 202-221, 1987								
C;Date: 23-Apr-1999 #sequence_revision 20-Aug-1999 #text_change 21-Jul-2000	A;Title: Ovomucoid third domains from 100 avian species: isolation, sequences, and hy									
R;Gray, J.; Close, P.S.; Briggs, S.P.; Johal, G.S.	A;Reference Number: R90515; MUID:81157615									
Cell 89, 25-31, 1997	A;Accession: B31443									
A;Title: A novel suppressor of cell death in plants encoded by the l1sl gene of maize.	A;Molecule type: protein									
A;Reference number: Z15232; MUID:97248483	A;Residues: 1-54 <IaS>									
A;Accession: T04136	A;Note: the authors designate this sequence with the code OMAH3									
A;Molecule type: DNA	C;Superfamily: ovomucoid; Kazal protease inhibitor homology									
A;Residues: 1-505 <GRA>	C;Keywords: egg white, glycoprotein, serine proteinase inhibitor									
A;Cross-references: EMBL:077346; NID:91935910; PIDN: AAC49678.1; PID:91935912	F;4-54/Domain: Kazal protease inhibitor homology <KPI>									
A;Status: preliminary; translated from GB/EMBL/DDBJ	F;6-36, 14-33, 22-54/disulfide bonds: #status predicted									
A;Molecule type: mRNA	F;43/Binding site: carbohydrate (Asn) (covalent) #status experimental									
A;Residues: 54-403, 'P', 405-443, 'HT', 446-497, 'V', 499-520 <GRA>										
A;Cross-references: EMBL:077345; NID:91935908; PIDN: AAC49676.1; PID:91935909										
A;Experimental source: strain pa405 inbred line; leaf										
C;Genetics:										
A;Gene: l1sl										
A;Map position: 1S										
A;Introns: 123/3; 202/2; 244/3; 290/2; 343/3; 436/3										
C;Superfamily: Rieske [2Fe-2S] homology										
C;Keywords: Rieske [2Fe-2S]; metalloprotein; Rieske iron-sulfur protein										
F;115, 117, 135, 138/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status F										
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Best Local Similarity	100.0%;	Pred. No. 8.1;								
Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	148 PTQEALPS 155									
Db	422 PTQEALPS 429									
RESULT	8									
T08423	Axin homolog Axil - rat	RESULT	10							
C;Species: Rattus norvegicus (Norway rat)	H61588	ovomucoid (PSTI-type proteinase inhibitor), third domain - hoatzin	C;Species: Opithocomus hoazin (hoatzin)	C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 17-Mar-1999						
C;Accession: T08423	C;Accession: H61588; A41435	R;Laskowski Jr., M.; Apostol, I.; Gileto, A.; Komiyama, T.; Zhang, W.; Laskowski Jr., M.								
C;Date: 05-Nov-1999 #sequence_revision 21-Jul-2000	J. Protein Chem. 12, 419-433, 1993									
C;Accession: T08423	A;Title: Amino acid sequences of ovomucoid third domains from 27 additional species o									
C;Accession: T08423	A;Reference Number: A61587; MUID:94072078									
C;Accession: H61588	A;Accession: H61588									
C;Accession: H61588	A;Molecule type: protein									
C;Accession: H61588	A;Residues: 1-54 <APo>									
C;Accession: H61588	C;Superfamily: ovomucoid; Kazal protease inhibitor homology <KPI>									
C;Accession: H61588	C;Keywords: serine proteinase inhibitor									
C;Accession: H61588	F;4-54/Domain: Kazal protease inhibitor homology <KPI>									
C;Accession: H61588	F;6-36, 14-33, 22-54/disulfide bonds: #status predicted									
Query Match	4.9%; Score 7; DB 2;	Length 54;								
Best Local Similarity	100.0%;	Pred. No. 8.1;								
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	49 NGTISLS 55									
Db	43 NGTISLS 49									
RESULT	11									
T49624	hypothetical protein B5022.60 [imported] - Neurospora crassa	C;Species: Neurospora crassa	C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000							
C;Accession: T49624	C;Accession: T49624									
C;Accession: T49624	R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu									
Query Match	4.9%; score 8; DB 2;	Length 838;								
Best Local Similarity	100.0%;	Pred. No. 7.6;								

C;Note: interacts with GSK-3beta and beta-catenin

C;Keywords: phosphoprotein; signal transduction

submitted to the Protein Sequence Database, May 2000  
 A; Reference number: 225022

A; Accession: T45624  
 A; Status: preliminary

A; Molecule type: DNA  
 A; Cross-references: EMBL:AL135932; GSPDB:GN00116; NCSP:B5022.60

A; Experimental source: BAC clone B5022; strain OR/4A

C; Genetics:  
 A; Gene: NCSP:B5022.60

A; Map position: 6  
 C; Superfamily: Neurospora crassa hypothetical protein B5022.60

Query Match 4.3%; Score 7; DB 2; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 59 CSRFPNF 65  
 Db 30 CSRFPNF 36

RESULT 12  
 F83531 hypothetical protein PA0907 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C; Species: Pseudomonas aeruginosa  
 C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C; Accession: F83531  
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Britton, S.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A; Reference number: A82950; MUID:20437337  
 A; Accession: F83531  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-176 <S0>  
 A; Cross-references: GB:AE004525; GB:AE004091; NID:99946805; PIDN:AAG04296.1; GSPDB:GN001  
 A; Experimental source: strain PA01  
 C; Genetics:  
 A; Gene: PA0907

Query Match 4.3%; Score 7; DB 2; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 59 CSRFPNF 65  
 Db 30 CSRFPNF 36

RESULT 14  
 A70421 fructose-1,6-bisphosphate aldolase class II - Aquifex aeolicus  
 C; Species: Aquifex aeolicus  
 C; Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 22-Jun-1999  
 C; Accession: A70421  
 R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.; Nature 392, 353-358, 1998  
 A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A; Reference number: A70300; MUID:96196656  
 A; Accession: A70421  
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-310 <S0>  
 A; Cross-references: GB:AE000737; NID:g2983782; PIDN: AAC07345.1; PID:92983787; GH:AE00  
 A; Experimental source: strain VF5  
 C; Genetics:  
 C; Gene: fba  
 C; Superfamily: fructose-bisphosphate aldolase II

Query Match 4.3%; Score 7; DB 2; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 75 SFIEHLPL 81  
 Db 40 SFIEHLPL 46

RESULT 15  
 S37595 mucin JU110 - human (fragment)  
 C; Species: Homo sapiens (man)  
 C; Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
 C; Accession: S37595; S35048  
 R; Aubert, J.  
 Submitted to the EMBL Data Library, September 1993  
 A; Reference number: S37593  
 A; Accession: S37595  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-330 <S0>  
 A; Cross-references: EMBL:X74956; NID:9407052; PIDN:CAA52911.1; PID:9407053  
 R; Dutfosse, J.; Porchet, N.; Audie, J.P.; Guyonnet-Duperat, V.; Laine, A.; van Seuningen, Biochem. J. 293, 329-337, 1993  
 A; Title: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic alternations  
 A; Accession: S35048  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-330 <S0>

Query Match 4.3%; Score 7; DB 2; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 6 TTATAA 12  
 Db 4 TTTATAA 12

RESULT 13  
 C70527 hypothetical protein Rv0330c - Mycobacterium tuberculosis (strain H37RV)  
 C; Species: Mycobacterium tuberculosis  
 C; Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C; Accession: C70527  
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A; Reference number: A70500; MUID:98295987  
 A; Accession: C70527  
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-146 <COL>  
 A; Cross-references: GB:Z96800; GB:AL123456; NID:93261800; PIDN:CA809578.1; PID:e321793;  
 A; Experimental source: strain H37RV

Wed Oct 9 15:32:10 2002

us-09-786-130-1.oligo.rpr

Page 5

Db 34 |||||  
TTAATA 40

Search completed: October 9, 2002, 02:25:38  
Job time: 5269 sec



OM protein - protein search, using sw model  
Run on: October 8, 2002, 22:31:48 ; Search time 19.91 Seconds  
Perfect score: 164  
Sequence: 1 TPVSOPTTAATASVRSTKDP..... TLPPPTQEALPSSHSSPQQQG 164  
Scoring table: OLIGO Gapop 60.0 , Gapext 60.0  
Searched: 231628 seqs, 24125594 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cn2\_6/podata/2/iaa/5A\_COMB.pep:\*

2: /cn2\_6/podata/2/iaa/5B\_COMB.pep:\*

3: /cn2\_6/podata/2/iaa/6A\_COMB.pep:\*

4: /cn2\_6/podata/2/iaa/6B\_COMB.pep:\*

5: /cn2\_6/podata/2/iaa/PCUTS\_COMB.pep:\*

6: /cn2\_6/podata/2/iaa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	4.9	520	4 US-08-810-009-2 Sequence 2, Appli
2	7	4.3	50	1 US-08-063-551A-2 Sequence 2, Appli
3	7	4.3	50	3 US-08-926-842B-50 Sequence 50, Appli
4	7	4.3	116	1 US-08-478-039-103 Sequence 103, Appli
5	7	4.3	116	1 US-08-477-349A-103 Sequence 13, Appli
6	7	4.3	275	2 US-08-578-709-13 Sequence 19, Appli
7	7	4.3	385	4 US-09-036-987A-19 Sequence 27, Appli
8	7	4.3	385	4 US-09-370-700-19 Sequence 25, Appli
9	7	4.3	403	4 US-08-861-774B-27 Sequence 15, Appli
10	7	4.3	406	4 US-08-861-774E-25 Sequence 1, Appli
11	7	4.3	407	4 US-08-861-774E-28 Sequence 5, Appli
12	7	4.3	500	2 US-08-578-709-15 Sequence 36, Appli
13	6	3.7	10	4 US-09-238-448-1 Sequence 38, Appli
14	6	3.7	10	4 US-09-238-448-5 Sequence 39, Appli
15	6	3.7	14	2 US-07-876-941B-36 Sequence 99, Appli
16	6	3.7	49	3 US-08-926-842B-49 Sequence 99, Appli
17	6	3.7	57	1 US-08-162-102C-38 Sequence 99, Appli
18	6	3.7	84	3 US-08-905-769-99 Sequence 99, Appli
19	6	3.7	84	3 US-08-905-616-99 Sequence 99, Appli
20	6	3.7	84	4 US-08-811-795-99 Sequence 99, Appli
21	6	3.7	84	4 US-08-639-075A-99 Sequence 99, Appli
22	6	3.7	84	4 US-09-124-311-99 Sequence 99, Appli
23	6	3.7	84	4 US-03-012-692-99 Sequence 99, Appli
24	6	3.7	84	4 US-08-905-613-99 Sequence 99, Appli
25	6	3.7	84	5 PCT-US95-1442A-99 Sequence 63, Appli
26	6	3.7	93	3 US-08-894-699-63 Sequence 63, Appli
27	3.7			4 US-09-444-410-63 Sequence 63, Appli

RESULT 1  
US 08-810-009-2  
; Sequence 2, Application US/08810009  
; Patent No. 6211437  
; GENERAL INFORMATION:  
; APPLICANT: Briggs, Steven P.  
; APPLICANT: Johal, Gurmukh S.  
; APPLICANT: Gray, John  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
; CELL DEATH AND DISEASE RESISTANCE IN PLANTS  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P. O. Drawer 34009  
; CITY: Charlotte  
; STATE: NC 28234  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810.009  
; FILING DATE: 04-MAR-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 321943  
; REFERENCE/DOCKET NUMBER: 5718-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 520 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-810-009-2

Query Match Best Local Similarity 4.9%; Score 8; DB 4; Length 520;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PROTEALPS 155

Db 422 PTQEALPS 429

STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

RESULT 2

US-08-063-551A-2

Sequence 2, Application US/08063551A

Patent No. 5,534,071

GENERAL INFORMATION:

APPLICANT: ROSENBERG, Eugene

TITLE OF INVENTION: Preparation exhibiting enzymatic

TITLE OF INVENTION: delignification activity, a method of

producing the same, and applications thereof

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BACON &amp; THOMAS

STREET: 625 Slatters Lane - 4th Floor

CITY: Alexandria

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 1.2Mb storage

OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/063,551A

FILING DATE: 10-SEP-1997

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 854,645

FILING DATE: 02-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Richard E. Fischer

REGISTRATION NUMBER: 26,382

REFERENCE/DOCKET NUMBER: RRF/Rosenberg/551

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-683-0500

TELEFAX: 703-683-1080

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

HYPOTHETICAL: NO

US-08-063-551A-2

RESULT 4

Query Match 4.3%; Score 7; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 5.5;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

QY	74 GSFIGHL 80
Db	24 GSFIGHL 30

Query Match 4.3%; Score 7; DB 3; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 5.5;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Sequence 103, Application US/08478039  
 Patent No. 5,681,722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992

PRIORITY APPLICATION DATA:

RESULT 3

US-08-926-842B-50

Sequence 50, Application US/08926842B

Patent No. 6,030,807

GENERAL INFORMATION:

APPLICANT: SA-NO. 6030807ueira, Isabel

APPLICANT: de Lencastre, Herminia

TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESS: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

APPLICATION NUMBER: US 07/856,281  
 FILING DATE: 23-MAR-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/735,064  
 FILING DATE: 25-JUL-1991  
 ATTORNEY /AGENT INFORMATION:  
 NAME: Teskin Esq., Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-161  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 103:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 116 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: Peptide  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE: Monkey  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT: #9  
 US-08-478-039-103

RESULT 5  
 US-08-476-349A-103  
 Sequence 103, Application US/08476349A  
 Patent No. 5750105  
 GENERAL INFORMATION:  
 APPLICANT: Newman, Roland A.  
 APPLICANT: Hanna, Nabil  
 APPLICANT: Raab, Ronald W.  
 TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
 NUMBER OF SEQUENCES: 114  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: 699 Prince St.  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/476,349A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/379,072  
 FILING DATE: 25-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/912,292  
 FILING DATE: 10-JUL-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/856,281  
 FILING DATE: 23-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/735,064  
 FILING DATE: 25-JUL-1991

ATTORNEY /AGENT INFORMATION:  
 NAME: Teskin Esq., Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-161  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 103:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 116 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: Peptide  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE: Monkey  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT: #9  
 US-08-476-349A-103

RESULT 6  
 US-08-578-709-13  
 Sequence 13, Application US/08578709  
 Patent No. 5814509  
 GENERAL INFORMATION:  
 APPLICANT: TANABE, Tadashi  
 TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/578,709  
 FILING DATE: 28-DEC-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/00838  
 FILING DATE: 27-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 114316/1994  
 FILING DATE: 28-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY /AGENT INFORMATION:  
 NAME: Gubinsky, Louis  
 REGISTRATION NUMBER: 24,835  
 REFERENCE/DOCKET NUMBER: Q40439  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)293-7860  
 TELEFAX: (202)293-7860  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 275 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-578-709-13

Query Match 4.3%; Score 7; DB 2; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 7  
US-09-036-987A-19  
Sequence 19, Application US/09036987A  
Patent NO. 6143526  
GENERAL INFORMATION:  
APPLICANT: Baltz, Richard H.  
APPLICANT: Broughton, Mary C.  
APPLICANT: Crawford, Kathryn P.  
APPLICANT: Madduri, Krishnamurthy  
; ; ;  
CURRENT FILING DATE: 1999-08-09  
EARLIER APPLICATION NUMBER: US 09/36987  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 385  
TYPE: PRT  
ORGANISM: Saccharopolyspora spinosa  
US-09-370-700-19

APPLICANT: Turner, Jan R.  
 APPLICANT: Waldron, Clive  
 TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
 TITLE OF INVENTION: Production  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dow AgroSciences LLC Patent Department  
 DB  
 Qy 123 VDPEQVW 129  
 |||||  
 A5 VDPEQVW 129  
 Query Match 4.3%; Score 7; DB 4; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

BB 45 VPPEQW 51

CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-09/036,987A  
FILING DATE: 09-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stuart, Donald R  
REGISTRATION NUMBER: 28,479  
REFERENCE/DOCKET NUMBER: 50,608  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317)337-4816  
TELEFAX: (317)337-4847  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
RESULT 9  
US-08/861-774E-27  
Sequence 27, Application US/08861774E  
Patent No. 6247007  
GENERAL INFORMATION:  
APPLICANT: Waters, Barbara  
APPLICANT: Miao, Vivian  
APPLICANT: Ho, Yap  
APPLICANT: Tong, Seow  
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR  
TITLE OF INVENTION: BIOACTIVE MOLECULES  
FILE REFERENCE: 9993-006  
CURRENT APPLICATION NUMBER: US/08/861,774E  
CURRENT FILING DATE: 1997-05-22  
NUMBER OF SEQ ID NOS: 94  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 27  
LENGTH: 403  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: KS beta gene  
US-08/861-774E-27

Query	Match	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
Best Local Similarity	4.3%	Score 7;	DB 4;	78	EHLPGRL	0	0;	0;
Pred. No.	100.0%	Length 385;	78		84	0;	0;	0;
Matches	7;	Indels	59	EHLPGRL	65	0;	0;	0;
Conservative	0;	Mismatches	59	EHLPGRL	65	0;	0;	0;

Db 45 VDPEQVW 5:

RESULT 8  
US-09-370-700-19  
; Sequence 19, Application US/09370700  
• Patent No. 6274350



Db 5 CSRFPN 10

RESULT 14

US-09-238-448-5

; Sequence 5, Application US/09238448

; Patent No. 6238925

; GENERAL INFORMATION:

; APPLICANT: Sampson, Hugh A.

; TITLE OF INVENTION: Method for Determining Likelihood of Developing

; FILE REFERENCE: HS 100

; CURRENT APPLICATION NUMBER: US/09/238,448

; FILING DATE: 1999-01-28

; EARLIER APPLICATION NUMBER: 60/073,171

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: peptide

; US-09-238-448-5

Query Match

Best Local Similarity

3.7%; Score 6; DB 4;

Length 10;

Matches

6; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Oy

59 CSRFPN 64

||||||

Db

3 CSRFPN 8

RESULT 15

US-07-876-941A-36

; Sequence 36, Application US/07876941A

; Patent No. 5885768

; GENERAL INFORMATION:

; APPLICANT: Reyes, Gregory R.

; APPLICANT: Bradley, Daniel W.

; APPLICANT: Tam, Albert W.

; APPLICANT: Mitchell, Carl

; TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger &amp; Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/876,941A

; FILING DATE: 01-MAY-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 822,335

; FILING DATE: 17-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 505,888

; FILING DATE: 05-APRIL-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 420,921

; FILING DATE: 13-OCTOBER-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 367,486

; FILING DATE: 16-JUNE-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 336,672

; FILING DATE: 11-APRIL-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 208,997

; FILING DATE: 17-JUNE-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 4500-0093.33

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0960

; TELEX/FAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: FIG. 11, ORF 2, aa 341-354

; US-07-876-941A-36

Search completed: October 9, 2002, 01:47:15

Job time: 11727 sec

Query Match

Best Local Similarity

3.7%; Score 6; DB 2;

Length 14;

Matches

6; Conservative

0; Mismatches

0; Indels

0; Gaps

Oy

6 TTTAAT 11

||||||

Db

2 TTTAAT 7